



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Shiver, John W
Liu, Margaret A
Perry, Helen C

(ii) TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION

(iii) NUMBER OF SEQUENCES: 100

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Rahway
(D) STATE: New Jersey
(E) COUNTRY: United States of America
(F) ZIP: 07065

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/393,803
(B) FILING DATE: 9/10/99
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hand, J. Mark
(B) REGISTRATION NUMBER: 36,545
(C) REFERENCE/DOCKET NUMBER: 19188Y

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly	Pro
1				5					10					15	
Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Gly	Glu	Ile	Ile	Gly	Asp	Ile	Arg	Gln
			20					25					30		
Ala	His	Cys													
		35													

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys	Thr	Arg	Pro	Asn	Tyr	Asn	Lys	Arg	Lys	Arg	Ile	His	Ile	Gly	Pro
1				5					10					15	
Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Lys	Asn	Ile	Ile	Gly	Thr	Ile	Arg	Gln
			20					25					30		
Ala	His	Cys													
		35													

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg
1 5 10 15

Gly Pro Gly Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg
20 25 30

Gln Ala His Cys
35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro
1 5 10 15

Gly Arg Ala Phe Tyr Thr Thr Gly Lys Ile Ile Gly Asn Ile Arg Gln
20 25 30

Ala His Cys
35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys	Thr	Arg	Pro	Ser	Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	His	Ile	Gly
1				5					10					15	
Pro	Gly	Lys	Ala	Phe	Tyr	Ala	Thr	Gly	Ala	Ile	Ile	Gly	Asp	Ile	Arg
			20					25					30		
Gln	Ala	His	Cys												
			35												

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Arg	Ser	Ile	His	Ile	Ala	Pro
1				5					10					15	
Gly	Arg	Ala	Phe	Tyr	Ala	Thr	Gly	Asp	Ile	Ile	Gly	Asp	Ile	Arg	Gln
			20					25					30		
Ala	His	Cys													
			35												

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTATATAAGC AGAGCTCGTT TAG 23

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTAGCAAAGA TCTAAGGACG GTGACTGCAG 30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTATGTGTCT GAAAATGAGC GTGGAGATTG GGCTCGCAC 39

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGCGAGCCC AATCTCCACG CTCATTTTCA GACACATAC

39

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTACAAGAT CTACTATAGG GAGACCGGAA TTCCGC

36

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCG	GAGACGGTCA	60
CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG	120
TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	180
ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGATTGG	240
CTATTGGCCA	TTGCATACGT	TGTATCCATA	TCATAATATG	TACATTTATA	TTGGCTCATG	300
TCCAACATTA	CCGCCATGTT	GACATTGATT	ATTGACTAGT	TATTAATAGT	AATCAATTAC	360
GGGGTCATTA	GTTCATAGCC	CATATATGGA	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	420
CCCGCCTGGC	TGACCGCCCA	ACGACCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	480
CATAGTAACG	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGAGTATT	TACGGTAAAC	540
TGCCCCACTTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	ACGCCCCCTA	TTGACGTCAA	600
TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG	ACCTTATGGG	ACTTTCCTAC	660
TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	TATTACCATG	GTGATGCGGT	TTTGGCAGTA	720
CATCAATGGG	CGTGGATAGC	GGTTTGACTC	ACGGGGATTT	CCAAGTCTCC	ACCCCATTGA	780
CGTCAATGGG	AGTTTGTTTT	GGCACCAAAA	TCAACGGGAC	TTTCCAAAAT	GTCGTAACAA	840
CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	900
AGCTCGTTTA	GTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	960
TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCGTGCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCCA	CCCCCTTGGC	1080
TTCTTATGCA	TGCTATACTG	TTTTTGGCTT	GGGGTCTATA	CACCCCCGCT	TCCTCATGTT	1140
ATAGGTGATG	GTATAGCTTA	GCCTATAGGT	GTGGGTATT	GACCATTATT	GACCACTCCC	1200
CTATTGGTGA	CGATACTTTC	CATTACTAAT	CCATAACATG	GCTCTTTGCC	ACAACTCTCT	1260
TTATTGGCTA	TATGCCAATA	CACGTGCCTT	CAGAGACTGA	CACGGACTCT	GTATTTTTAC	1320
AGGATGGGGT	CTCATTTATT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
CCGCAGTTTT	TATTAAACAT	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCGGG	1440
ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC	TTCTACATCC	GAGCCCTGCT	CCCATGCCTC	1500
CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GCTCCTAACA	GTGGAGGCCA	GACTTAGGCA	1560
CAGCACGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCGGTAG	GGTATGTGTC	1620

TGAAAATGAG	CTCGGGGAGC	GGGCTTGCAC	CGCTGACGCA	TTTGAAGAC	TTAAGGCAGC	1680
GGCAGAAGAA	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAAGTCC	1740
CGTTGCGGTG	CTGTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCGC	1800
GCGCGCCACC	AGACATAATA	GCTGACAGAC	TAACAGACTG	TTCTTTTCCA	TGGGTCTTTT	1860
CTGCAGTCAC	CGTCCCTAGA	TCTGCTGTGC	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	1920
CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	1980
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	2040
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	2100
GCTCTATGGG	TACCCAGGTG	CTGAAGAATT	GACCCGGTTC	CTCCTGGGCC	AGAAAAGAAGC	2160
AGGCACATCC	CCTTCTCTGT	GACACACCTT	GTCCACGCCC	CTGGTTCTTA	GTTCCAGCCC	2220
CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTAC	2280
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2400
TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
CGCTCGGTCTG	TTCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580
AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2640
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700
CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	2760
GGATACCTGT	CEGCCTTTCT	CCCTTCGGGA	AGCGTGCGC	TTTCTCAATG	CTCACGCTGT	2820
AGGTATCTCA	GTTGCGTGTA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	2880
GTTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	AACTATCGTC	TTGAGTCCAA	CCCGGTAAGA	2940
CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	3000
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	3060
TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	3180
CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	3240

TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	3300
TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	3360
TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	3420
CGTTCATCCA	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA	3480
CCATCTGGCC	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	GCTCACCGGC	TCCAGATTTA	3540
TCAGCAATAA	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	GTGGTCCTGC	AACTTTATCC	3600
GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	GAAGCTAGAG	TAAGTAGTTC	GCCAGTTAAT	3660
AGTTTGCGCA	ACGTTGTTGC	CATTGCTACA	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	3720
ATGGCTTCAT	TCAGTCCGG	TTCCCAACGA	TCAAGGCGAG	TTACATGATC	CCCCATGTTG	3780
TGCAAAAAG	CGGTTAGCTC	CTTCGGTCTT	CCGATCGTTG	TCAGAAGTAA	GTTGGCCGCA	3840
GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	CATAATTCTC	TTACTGTCAT	GCCATCCGTA	3900
AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	3960
CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	CGGGATAATA	CCGCGCCACA	TAGCAGAACT	4020
TTAAAAGTGC	TCATCATTTG	AAAACGTTCT	TCGGGGCGAA	AACTCTCAAG	GATCTTACCG	4080
CTGTTGAGAT	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA	ACTGATCTTC	AGCATCTTTT	4140
ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC	AAAAAAGGGA	4200
ATAAGGGCGA	CACGGAAATG	TTGAATACTC	ATACTCTTCC	TTTTTCAATA	TTATTGAAGC	4260
ATTTATCAGG	GTTATTGTCT	CATGAGCGGA	TACATATTTG	AATGTATTTA	GAAAAATAAA	4320
CAAATAGGGG	TTCCGCGCAC	ATTTCCCCGA	AAAGTGCCAC	CTGACGTCTA	AGAAACCATT	4380
ATTATCATGA	CATTAACCTA	TAAAAATAGG	CGTATCACGA	GGCCCTTTCG	TC	4432

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATTGGCTATT GGCCATTGCA TACGTTGTAT CCATATCATA ATATGTACAT TTATATTGGC	60
TCATGTCCAA CATTACCGCC ATGTTGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA	120
ATTACGGGGT CATTAGTTCA TAGCCCATAT ATGGAGTTCC GCGTTACATA ACTTACGGTA	180
AATGGCCCCG CTGGCTGACC GCCCAACGAC CCCCGCCCAT TGACGTCAAT AATGACGTAT	240
GTTCCCATAG TAACGCCAAT AGGGACTTTC CATTGACGTC AATGGGTGGA GTATTTACGG	300
TAAACTGCCC ACTTGGCAGT ACATCAAGTG TATCATATGC CAAGTACGCC CCCATATTGAC	360
GTCAATGACG GTAAATGGCC CGCCTGGCAT TATGCCCAGT ACATGACCTT ATGGGACTTT	420
CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGTGAT GCGGTTTTTG	480
CAGTACATCA ATGGGCGTGG ATAGCGGTTT GACTCACGGG GATTTCCAAG TCTCCACCCC	540
ATTGACGTCA ATGGGAGTTT GTTTTGGCAC CAAAATCAAC GGGACTTTCC AAAATGTCGT	600
AACAACCTCCG CCCCATTGAC GCAAATGGGC GGTAGGCGTG TACGGTGGGA GGCTATATA	660
AGCAGAGCTC GTTTAGTGAA CCGTCAGATC GCCTGGAGAC GCCATCCACG CTGTTTTGAC	720
CTCCATAGAA GACACCGGGA CCGATCCAGC CTCCGCGGCC GGAACGGTG CATTGGAACG	780
CGGATTCCCC GTGCCAAGAG TGACGTAAGT ACCGCTATA GAGTCTATAG GCCACCCCC	840
TTGGCTTCTT ATGCATGCTA TACTGTTTTT GGCTTGGGGT CTATACACCC CCGCTTCCTC	900
ATGTTATAGG TGATGGTATA GCTTAGCCTA TAGGTGTGGG TTATTGACCA TTATTGACCA	960
CTCCCCTATT GGTGACGATA CTTTCCATTA CTAATCCATA ACATGGCTCT TTGCCACAAC	1020
TCTCTTTATT GGCTATATGC CAATACACTG TCCTTCAGAG ACTGACACGG ACTCTGTATT	1080
TTTACAGGAT GGGGTCTCAT TTATTATTTA CAAATTCACA TATACAACAC CACCGTCCCC	1140
AGTGCCCGCA GTTTTTATTA AACATAACGT GGGATCTCCA CGCGAATCTC GGTACGTGT	1200
TCCGGACATG GGCTCTTCTC CGGTAGCGGC GGAGCTTCTA CATCCGAGCC CTGCTCCCAT	1260
GCCTCCAGCG ACTCATGGTC GCTCGGCAGC TCCTTGCTCC TAACAGTGGA GGCCAGACTT	1320
AGGCACAGCA CGATGCCCAC CACCACCAGT GTGCCGCACA AGGCCGTGGC GGTAGGGTAT	1380
GTGTCTGAAA ATGAGCTCGG GGAGCGGGCT TGCACCGCTG ACGCATTTGG AAGACTTAAG	1440
GCAGCGGCAG AAGAAGATGC AGGCAGCTGA GTTGTTGTGT TCTGATAAGA GTCAGAGGTA	1500
ACTCCCGTTG CGGTGCTGTT AACGGTGGAG GGCAGTGTAG TCTGAGCAGT ACTCGTTGCT	1560

GCCGCGCGCG	CCACCAGACA	TAATAGCTGA	CAGACTAACA	GACTGTTCCCT	TTCCATGGGT	1620
CTTTTCTGCA	GTCACCGTCC	TTAGATCTGC	TGTGCCTTCT	AGTTGCCAGC	CATCTGTTGT	1680
TTGCCCCCTCC	CCCGTGCCCT	CCTTGACCCT	GGAAGGTGCC	ACTCCCCTG	TCCTTTCCTA	1740
ATAAAATGAG	GAAATTGCAT	CGCATTGTCT	GAGTAGGTGT	CATTCTATTC	TGGGGGGTGG	1800
GGTGGGGCAG	CACAGCAAGG	GGGAGGATTG	GGAAGACAAT	AGCAGGCATG	CTGGGGATGC	1860
GGTGGGCTCT	ATGGGTACCC	AGGTGCTGAA	GAATTGACCC	GGTTCCTCCT	GGGCCAGAAA	1920
GAAGCAGGCA	CATCCCCTTC	TCTGTGACAC	ACCCTGTCCA	CGCCCCTGGT	TCTTAGTTCC	1980
AGCCCCACTC	ATAGGACACT	CATAGCTCAG	GAGGGCTCCG	CCTTCAATCC	CACCCGCTAA	2040
AGTACTTGGA	GCGGTCTCTC	CCTCCCTCAT	CAGCCCACCA	AACCAAACCT	AGCCTCCAAG	2100
AGTGGAAGA	AATTAAAGCA	AGATAGGCTA	TTAAGTGCAG	AGGGAGAGAA	AATGCCTCCA	2160
ACATGTGAGG	AAGTAATGAG	AGAAATCATA	GAATTC			2196

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGTCCCCG	GAGACGGTCA	60
CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCCG	TCAGGGCGCG	TCAGCGGGTG	120
TTGGCGGGTG	TCGGGGCTGG	CTTAACATATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	180
ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGATTGG	240
CTATTGGCCA	TTGCATACGT	TGTATCCATA	TCATAATATG	TACATTTATA	TTGGCTCATG	300
TCCAACATTA	CCGCCATGTT	GACATTGATT	ATTGACTAGT	TATTAATAGT	AATCAATTAC	360
GGGGTCATTA	GTTCATAGCC	CATATATGGA	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	420
CCCGCCTGGC	TGACCGCCCA	ACGACCCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	480

CATAGTAACG	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGAGTATT	TACGGTAAAC	540
TGCCCCACTTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	ACGCCCCCTA	TTGACGTCAA	600
TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG	ACCTTATGGG	ACTTTCCTAC	660
TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	TATTACCATG	GTGATGCGGT	TTTGGCAGTA	720
CATCAATGGG	CGTGGATAGC	GGTTTGACTC	ACGGGGATTT	CCAAGTCTCC	ACCCCATTGA	780
CGTCAATGGG	AGTTTGTTTT	GGCACCAAAA	TCAACGGGAC	TTTCCAAAAT	GTCGTAACAA	840
CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	900
AGCTCGTTTA	GTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	960
TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCGTGCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCCA	CCCCCTTGGC	1080
TTCTTATGCA	TGCTATACTG	TTTTTGGCTT	GGGGTCTATA	CACCCCCGCT	TCCTCATGTT	1140
ATAGGTGATG	GTATAGCTTA	GCCTATAGGT	GTGGGTTATT	GACCATTATT	GACCACTCCC	1200
CTATTGGTGA	CGATACTTTC	CATTACTAAT	CCATAACATG	GCTCTTTGCC	ACAACCTCTCT	1260
TTATTGGCTA	TATGCCAATA	CACTGTCCTT	CAGAGACTGA	CACGGACTCT	GTATTTTTTAC	1320
AGGATGGGGT	CTCATTTATT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
CCGCAGTTTT	TATTAAACAT	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCGGG	1440
ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC	TTCTACATCC	GAGCCCTGCT	CCCATGCCTC	1500
CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GCTCCTAACA	GTGGAGGCCA	GACTTAGGCA	1560
CAGCACGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCGGTAG	GGTATGTGTC	1620
TGAAAATGAG	CTCGGGGAGC	GGGCTTGAC	CGCTGACGCA	TTTGGAAGAC	TTAAGGCAGC	1680
GGCAGAAGAA	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAACCTC	1740
CGTTGCGGTG	CTGTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCGC	1800
GCGCGCCACC	AGACATAATA	GCTGACAGAC	TAACAGACTG	TTCTTTTCCA	TGGGTCTTTT	1860
CTGCAGTCAC	CGTCCTTAGA	TCTGCTGTGC	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	1920
CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACTGTCCTT	TCCTAATAAA	1980
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	2040
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	2100

GCTCTATGGG	TACCCAGGTG	CTGAAGAATT	GACCCGGTTC	CTCCTGGGCC	AGAAAGAAGC	2160
AGGCACATCC	CCTTCTCTGT	GACACACCCT	GTCCACGCCC	CTGGTTCTTA	GTTCCAGCCC	2220
CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTAC	2280
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAAATGC	CTCCAACATG	2400
TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
CGCTCGGTCTG	TTCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580
AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2640
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700
CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	2760
GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	2820
AGGTATCTCA	GTTGCGTGTA	GGTCGTTTCG	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	2880
GTTTCAGCCG	ACCGCTGCGC	CTTATCCGGT	AACATATCGTC	TTGAGTCCAA	CCCGGTAAGA	2940
CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	3000
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	3060
TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	3180
CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	3240
TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	3300
TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	3360
TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	3420
CGTTCATCCA	TAGTTGCCTG	ACTCCGGGGG	GGGGGGGCGC	TGAGGTCTGC	CTCGTGAAGA	3480
AGGTGTTGCT	GACTCATACC	AGGCCTGAAT	CGCCCCATCA	TCCAGCCAGA	AAGTGAGGGA	3540
GCCACGGTTG	ATGAGAGCTT	TGTTGTAGGT	GGACCAGTTG	GTGATTTTGA	ACTTTTGCTT	3600
TGCCACGGAA	CGGTCTGCGT	TGTCGGGAAG	ATGCGTGATC	TGATCCTTCA	ACTCAGCAAA	3660
AGTTCGATTT	ATTCAACAAA	GCCGCCGTCC	CGTCAAGTCA	GCGTAATGCT	CTGCCAGTGT	3720
TACAACCAAT	TAACCAATTC	TGATTAGAAA	AACTCATCGA	GCATCAAATG	AAACTGCAAT	3780

TTATTCATAT CAGGATTATC AATACCATAT TTTTGAAAAA GCCGTTTCTG TAATGAAGGA	3840
GAAAACTCAC CGAGGCAGTT CCATAGGATG GCAAGATCCT GGTATCGGTC TGCATTCCG	3900
ACTCGTCCAA CATCAATACA ACCTATTAAT TTCCCCTCGT CAAAAATAAG GTTATCAAGT	3960
GAGAAATCAC CATGAGTGAC GACTGAATCC GGTGAGAATG GCAAAAGCTT ATGCATTTCT	4020
TTCCAGACTT GTTCAACAGG CCAGCCATTA CGCTCGTCAT CAAAATCACT CGCATCAACC	4080
AAACCGTTAT TCATTTCGTGA TTGCGCCTGA GCGAGACGAA ATACGCGATC GCTGTTAAAA	4140
GGACAATTAC AAACAGGAAT CGAATGCAAC CGGCGCAGGA AACTGCCAG CGCATCAACA	4200
ATATTTTCAC CTGAATCAGG ATATTCCTCT AATACCTGGA ATGCTGTTTT CCCGGGGATC	4260
GCAGTGGTGA GTAACCATGC ATCATCAGGA GTACGGATAA AATGCTTGAT GGTCGGAAGA	4320
GGCATAAATT CCGTCAGCCA GTTTAGTCTG ACCATCTCAT CTGTAACATC ATTGGCAACG	4380
CTACCTTTGC CATGTTTCAG AAACAACCTCT GGCGCATCGG GCTTCCCATA CAATCGATAG	4440
ATTGTGCGAC CTGATTGCCC GACATTATCG CGAGCCCATT TATACCCATA TAAATCAGCA	4500
TCCATGTTGG AATTTAATCG CGGCCTCGAG CAAGACGTTT CCCGTTGAAT ATGGCTCATA	4560
ACACCCCTTG TATTACTGTT TATGTAAGCA GACAGTTTTA TTGTTTCATGA TGATATATTT	4620
TTATCTTGTG CAATGTAACA TCAGAGATTT TGAGACACAA CGTGGCTTTC CCCCCCCCCC	4680
CATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT	4740
TAGAAAAATA AACAAATAGG GGTCCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC	4800
TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAATA GGCGTATCAC GAGGCCCTTT	4860
CGTC	4864

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACATAGAT CTGTTCCATG GTTGTGGCAA TATTATCATC G

41

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTACAAGAT CTACCATGGC AGGAAGAAGC GGAGACAGC

39

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACATAGAT CTGATATCGC ACTATTCTTT AGCTCCTGAC TCC

43

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATCACCATG GATGCAATGA AGAGAGGGCT CTGCTGTGTG CTGCTGCTGT GTGGAGCAGT 60
CTTCGTTTCG CCCAGCGA 78

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATCTCGCTG GGCGAAACGA AGACTGCTCC ACACAGCAGC AGCACACAGC AGAGCCCTCT 60
CTTCATTGCA TCCATGGT 78

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTACATGAT CAGATATCGC CCGGGCCGAG ATCTTCAGAC TTGGAGGAGG AG 52

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCACATTGAT CAGCTTGTGT AATTGTTAAT TTCTCTGTCC

40

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCCGGATCC TGATCACAGA AAAATTGTGG GTCACAGTC

39

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCCCAGGAAT CCACCTGTTA GCGCTTTTCT CTCTGCACCA CTCTTCTC

48

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGTACATGAT CACAGAAAAA TTGTGGGTCA CAGTC

35

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCACATTGAT CAGATATCTT ATCTTTTTTC TCTCTGCACC ACTCTTC

47

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCACCGTCC TCTATCAAAG CAGTAAGTAG TACATGCA

38

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGTACTACTT ACTGCTTTGA TAGAGGACGG TGACTGCA

38

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGTACATGAT CAACCATGAG AGTGAAGGAG AAATATCAGC

40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCACATTGAT CAGATATCCC CATCTTATAG CAAAATCCTT TCC

43

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCACATTGAT CAGATATCCC CATCTTATAG CAAAATCCTT TCC

43

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTACACTGC AGTCACCGTC CTATGGCAGG AAGAAGCGGA GAC

43

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCACATCAGG TACCCCATAA TAGACTGTGA CC

32

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACAAGAT CTACCATGGG ACCAGTACAA CAAATAGGTG GTAAC

45

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCACATAGAT CTTTACATTA ATCTAGCCTT CTGTCCC

37

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTACAACCA TGGGTGGAGC TATTTCCATG AGG

33

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCTAGGTTAG CCTTCTTCTA ACCTCTTCC

29

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTACAAGAT CTACCATGGG ATGTCTTGGG AATCAGC

37

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCACATAGAT CTGATATCGT ATGAGTCTAC TGGAAATAAG AGG

43

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGTACAGGAT CCACCATGGG TGCGAGAGCG TCAGTATTAA GC

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCACATGGAT CCGCCCGGGC TTACATCTCT GTACAAATTT CTACTAATGC

50

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGTACAGGAT CCCCCGCACGG CAAGAGGCGA GGG

33

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGTACAGGAT CCACCATGGC TGCGAGAGCG TCAGTATTAA GC

42

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCACATGGAT CCGCCCGGGC CTTTATTGTG ACGAGGGGTC GTTGC

45

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTACAGGAT CCCCCGACGG CAAGAGGCGA GGG

33

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGTACAGGAT CCACCATGGC TGCGAGAGCG TCAGTATTAA GC

42

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTACCTCATG AGCCACATAA TACCATG

27

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTACAAGAT CTACCATGGC TTGCAATTGT CAGTTGATGC

40

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CCACATAGAT CTCCATGGGA ACTAAAGGAA GACGGTCTGT TC

42

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGTACAAGAT CTACCATGAA GGCAAACCTA CTGGTCCTG

39

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCACATAGAT CTGATATCCT AATCTCAGAT GCATATTCTG CACTGC

46

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Arg	Ile	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Thr	Thr	Lys	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAAAGAGCAG AAGACAGTGG CAATGA

26

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGGCTTTGCT AAATGGGTGG CAAGTGGCCC GGGCATGTGG

40

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTAACAGACT GTTCCTTTCC ATG

23

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGAGTGGCAC CTTCCAGG

18

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGAGACAGCG ACGAAGACCT CCTCAAGGCA GTCAGACTCA TCAAG 45

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GATGGCTGGC AACTAGAAGG CACAGCAGAT CTGATATCGC ACTATTCTTT AGCTCCTGAC 60
TCCAATATTG T 71

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTTAGATCAA CCATGAGAGT GAAGGAGAAA TATCAGCACT TGTGGAGATG GGGGTGGAGA 60
TGGGGCACCA TGCTCCTTGG GATGTTGATG ATCTGTAGTG CTACAGAAAA ATTGTGGGT 119

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CTGGCAACTA GAAGGCACAG CAGATCAGAT AGTGTCCCCA TCTTATAGCA AAATCCTTTC 60

CAAGCCCTGT CTTATTCT 78

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GATTTAGGTG AACTATAG 19

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CATGCCTGCA GGTGACTCT AAATTCCG

28

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACCCGGGGAT CCTCTAGCGC GCTTGTCTCT TGTTCCA

37

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGGACGTGGT TTTCC

15

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TATGGCCACA ACCATGGCAG GAAGAAGCGG AGACAGCGAC GAAGACCTCC TCAAGGCAGT

60

CAGACT

66

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTCGAGCCAT GGGCCCCCTAG ACTATAGCGT GATAAGAAAT CGAGGACTGA GGTTATAACA

60

TCCTCTAAGG TGTTATAAAA CTCCCGAAGG

90

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCTTCGGCCA GTAACG

16

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTGCATGCCT GCAGGTGGTA CATGATCAGA TATCGCCCGG GCCGAGATCT TCAGACTTGG

60

AGGAGGAGAT ATGAGGGACA ATTGGAG

87

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGGGCGGAAT TTAGAGTCAA TTGATCAGCT TGTGTAATTG TTAATTTCTC TGTCCCACTC 60

CATCCAGGTC GTGTGATTC 79

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CCATCTCCAC AAGTGCTG 18

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGATCTAAGG ACGGTGACTG CATGTACTAC TTACTGCTTT GATAGAGGAC GGTGACTGCA 60

GAAAAGACCC ATGGAAA 77

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCTTCGGCCA GTAACG

16

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCACAGCAG ATCAGATGGG GATCTGATAT CGCACTATTC TTTAGCTCCT GACTCCTGAC

60

TC

62

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
GGAATTTGAG TCATCCCCAT CTTATAGCAA AATCCTTTCC AA 42

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
CTTAGATCCC CGCACGGCAA GAGGCGAGGG GCGGCGACTG GT 42

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
GGCACAGCAG ATCCGCCCGG GCTTACATCT CTGTACAAAT TTCTACTAAT GCTTTTATTT 60
TTCTTCTGTC 70

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTTAGATCCA CCATGGGTGC GAGAGCGTCA GTATTAAGCG GGGGGAGAAT TAGATCGATG	60
GGAAAAAATT	70

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCACAGCAG ATCCGCCCCG GCTTACATCT CTGTACAAAT TTCTACTAAT GCTTTTATTT	60
TTCTTCTGTC	70

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCACCGTCCT TAGATCACCA TGGATGCAAT GAAGAGAGGG CTCTGCTGTG TGCTGCTGCT 60

GTGTGGAGCA GTCTTCGTTT CGCCCAGCGA GATCTGCTGT GCCTTCTAGT TGCCAGCC 118

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTCGTTTCGC CCAGCGATCA CAGAAAAATT GTGGGTCACA GTC 43

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCACAGCAG ATCCACGTGT TAGCGCTTTT CTCTCTCCAC CAC 43

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCACCGTCCT TAGATCTACC ATGGGACCAG TACAACAAAT AGGTGGTAAC TATGTCCACC	60
TGCCATTAAG CCCGAGAACA	80

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGCACAGCAG ATCTTTACAT TAATCTAGCC TTCTGTCCCG GTCC	44
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(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCACCGTCCT TAGATCGGTA CAACCATGGG TGGAGCTATT TCCATGAGGC AATCCAAGCC	60
GGCTGGAGAT CTGACAGAAA	80

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGCACAGCAG ATCACCTAGG TTAGCCTTCT TCTAACCTCT TCCTCTGACA GGCCTGACTT	60
GCTTCCAACCT CTTCTGGGTA TCTAG	85

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACCGTCCTTA GATTGACAT AGCAGAATAG GCGTTACTCG ACAGAGGAGA GCAAGAAATG	60
GAGCCAGTAG ATCCTAGACT AGAGCCCTGG	90

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGCACAGCAG ATCCGAGATG CTGCTCCCAC CCCATCTGCT G

41

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Lys	Gln	Ile	Ile	Asn	Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

His	Glu	Asp	Ile	Ile	Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys
1				5					10			

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Asp	Arg	Val	Ile	Glu	Val	Val	Gln	Gly	Xaa	Tyr	Arg	Ala	Ile	Arg
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGTACAAATA TTGGCTATTG GCCATTGCAT ACG

33

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CCACATCTCG AGGAACCGGG TCAATTCTTC AGCACC

36

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGTACAGATA TCGGAAAGCC ACGTTGTGTC TCAAAATC

38

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCACATGGAT CCGTAATGCT CTGCCAGTGT TACAACC

37

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTACATGAT CACGTAGAAA AGATCAAAGG ATCTTCTTG

39

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CCACATGTCG ACCCGTAAAA AGGCCGCGTT GCTGG

35

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAGCCAATAT AAATGTAC

18

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CAATAGCAGG CATGC

15

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCAAGCAGCA GATTAC

16

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3547 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GATATTGGCT	ATTGGCCATT	GCATACGTTG	TATCCATATC	ATAATATGTA	CATTTATATT	60
GGCTCATGTC	CAACATTACC	GCCATGTTGA	CATTGATTAT	TGACTAGTTA	TTAATAGTAA	120
TCAATTACGG	GGTCATTAGT	TCATAGCCCA	TATATGGAGT	TCCGCGTTAC	ATAACTTACG	180
GTAAATGGCC	CGCCTGGCTG	ACCGCCCAAC	GACCCCCGCC	CATTGACGTC	AATAATGACG	240
TATGTTCCCA	TAGTAACGCC	AATAGGGACT	TTCCATTGAC	GTCAATGGGT	GGAGTATTTA	300
CGGTAAACTG	CCCCTTGGC	AGTACATCAA	GTGTATCATA	TGCCAAGTAC	GCCCCCTATT	360
GACGTCAATG	ACGGTAAATG	GCCCGCCTGG	CATTATGCCC	AGTACATGAC	CTTATGGGAC	420
TTTCCTACTT	GGCAGTACAT	CTACGTATTA	GTCATCGCTA	TTACCATGGT	GATGCGGTTT	480
TGGCAGTACA	TCAATGGGCG	TGGATAGCGG	TTTGACTCAC	GGGGATTTC	AAGTCTCCAC	540
CCCATTGACG	TCAATGGGAG	TTTGTTTTGG	CACCAAAATC	AACGGGACTT	TCCAAAATGT	600
CGTAACAAC	CCGCCCCATT	GACGCAAATG	GGCGGTAGGC	GTGTACGGTG	GGAGGTCTAT	660
ATAAGCAGAG	CTCGTTTAGT	GAACCGTCAG	ATCGCCTGGA	GACGCCATCC	ACGCTGTTTT	720
GACCTCCATA	GAAGACACCG	GGACCGATCC	AGCCTCCGCG	GCCGGGAACG	GTGCATTGGA	780
ACGCGGATTC	CCCGTGCCAA	GAGTGACGTA	AGTACCGCCT	ATAGAGTCTA	TAGGCCAC	840
CCCTTGGCTT	CTTATGCATG	CTATACTGTT	TTTGGCTTGG	GGTCTATACA	CCCCCGCTTC	900
CTCATGTTAT	AGGTGATGGT	ATAGCTTAGC	CTATAGGTGT	GGGTATTGA	CCATTATTGA	960
CCACTCCCC	ATTGGTGACG	ATACTTTCCA	TTACTAATCC	ATAACATGGC	TCTTTGCCAC	1020
AACTCTCTTT	ATTGGCTATA	TGCCAATACA	CTGTCTTCA	GAGACTGACA	CGGACTCTGT	1080
ATTTTTACAG	GATGGGGTCT	CATTTATTAT	TTACAAATTC	ACATATACAA	CACCACCGTC	1140
CCCAGTGCCC	GCAGTTTTTA	TTAAACATAA	CGTGGGATCT	CCACGCGAAT	CTCGGGTACG	1200
TGTTCCGGAC	ATGGGCTCTT	CTCCGGTAGC	GGCGGAGCTT	CTACATCCGA	GCCCTGCTCC	1260
CATGCCTCCA	GCGACTCATG	GTCGCTCGGC	AGCTCCTTGC	TCCTAACAGT	GGAGGCCAGA	1320
CTTAGGCACA	GCACGATGCC	CACCACCACC	AGTGTGCCGC	ACAAGGCCGT	GGCGGTAGGG	1380
TATGTGTCTG	AAAATGAGCT	CGGGGAGCGG	GCTTGCACCG	CTGACGCATT	TGGAAGACTT	1440
AAGGCAGCGG	CAGAAGAAGA	TGCAGGCAGC	TGAGTTGTTG	TGTTCTGATA	AGAGTCAGAG	1500
GTAACCTCCG	TTGCGGTGCT	GTTAACGGTG	GAGGGCAGTG	TAGTCTGAGC	AGTACTCGTT	1560
GCTGCCGCGC	GCGCCACCAG	ACATAATAGC	TGACAGACTA	ACAGACTGTT	CCTTTCCATG	1620

GGTCTTTTCT	GCAGTCACCG	TCCTTAGATC	TGCTGTGCCT	TCTAGTTGCC	AGCCATCTGT	1680
TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	CCTGGAAGGT	GCCACTCCCA	CTGTCCTTTC	1740
CTAATAAAAT	GAGGAAATTG	CATCGCATTG	TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	1800
TGGGGTGGGG	CAGCACAGCA	AGGGGGAGGA	TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	1860
TGCGGTGGGC	TCTATGGGTA	CGGCCGCAGC	GGCCGTACCC	AGGTGCTGAA	GAATTGACCC	1920
GGTTCCTCGA	CCCGTAAAAA	GGCCGCGTTG	CTGGCGTTTT	TCCATAGGCT	CCGCCCCCCT	1980
GACGAGCATC	ACAAAAATCG	ACGCTCAAGT	CAGAGGTGGC	GAAACCCGAC	AGGACTATAA	2040
AGATACCAGG	CGTTTCCCCC	TGGAAGCTCC	CTCGTGCCT	CTCCTGTTCC	GACCCTGCCG	2100
CTTACCGGAT	ACCTGTCCGC	CTTTCTCCCT	TCGGGAAGCG	TGGCGCTTTC	TCAATGCTCA	2160
CGCTGTAGGT	ATCTCAGTTC	GGTGTAGGTC	GTTTCCTCCA	AGCTGGGCTG	TGTGCACGAA	2220
CCCCCGTTTC	AGCCCGACCG	CTGCGCCTTA	TCCGGTAACT	ATCGTCTTGA	GTCCAACCCG	2280
GTAAGACACG	ACTTATCGCC	ACTGGCAGCA	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	2340
TATGTAGGCG	GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA	ACTACGGCTA	CACTAGAAGG	2400
ACAGTATTTG	GTATCTGCGC	TCTGCTGAAG	CCAGTTACCT	TCGGA AAAAG	AGTTGGTAGC	2460
TCTTGATCCG	GCAAACAAAC	CACCGCTGGT	AGCGGTGGTT	TTTTTGTTTG	CAAGCAGCAG	2520
ATTACGCGCA	GAAAAAAGG	ATCTCAAGAA	GATCCTTTGA	TCTTTTCTAC	GTGATCCCGT	2580
AATGCTCTGC	CAGTGTTACA	ACCAATTAAC	CAATTCTGAT	TAGAAAAACT	CATCGAGCAT	2640
CAAATGAAAC	TGCAATTTAT	TCATATCAGG	ATTATCAATA	CCATATTTTT	GAAAAAGCCG	2700
TTTCTGTAAT	GAAGGAGAAA	ACTCACCGAG	GCAGTTCCAT	AGGATGGCAA	GATCCTGGTA	2760
TCGGTCTGCG	ATTCCGACTC	GTCCAACATC	AATACAACCT	ATTAATTTCC	CCTCGTCAAA	2820
AATAAGGTTA	TCAAGTGAGA	AATCACCATG	AGTGACGACT	GAATCCGGTG	AGAATGGCAA	2880
AAGCTTATGC	ATTTCTTTCC	AGACTTGTTT	AACAGGCCAG	CCATTACGCT	CGTCATCAAA	2940
ATCACTCGCA	TCAACCAAAC	CGTTATTTCAT	TCGTGATTGC	GCCTGAGCGA	GACGAAATAC	3000
GCGATCGCTG	TTAAAAGGAC	AATTACAAAC	AGGAATCGAA	TGCAACCGGC	GCAGGAACAC	3060
TGCCAGCGCA	TCAACAATAT	TTTCACCTGA	ATCAGGATAT	TCTTCTAATA	CCTGGAATGC	3120
TGTTTTCCCG	GGGATCGCAG	TGGTGAGTAA	CCATGCATCA	TCAGGAGTAC	GGATAAAATG	3180
CTTGATGGTC	GGAAGAGGCA	TAAATTCCGT	CAGCCAGTTT	AGTCTGACCA	TCTCATCTGT	3240
AACATCATTG	GCAACGCTAC	CTTTGCCATG	TTTCAGAAAC	AACTCTGGCG	CATCGGGCTT	3300

CCCATACAAT	CGATAGATTG	TCGCACCTGA	TTGCCCAGACA	TTATCGCGAG	CCCATTATA	3360
CCCATATAAA	TCAGCATCCA	TGTTGGAATT	TAATCGCGGC	CTCGAGCAAG	ACGTTTCCCG	3420
TTGAATATGG	CTCATAACAC	CCCTTGATT	ACTGTTTATG	TAAGCAGACA	GTTTTATTGT	3480
TCATGATGAT	ATATTTTAT	CTTGTGCAAT	GTAACATCAG	AGATTTTGAG	ACACAACGTG	3540
GCTTTCC						3547